Fig. 1

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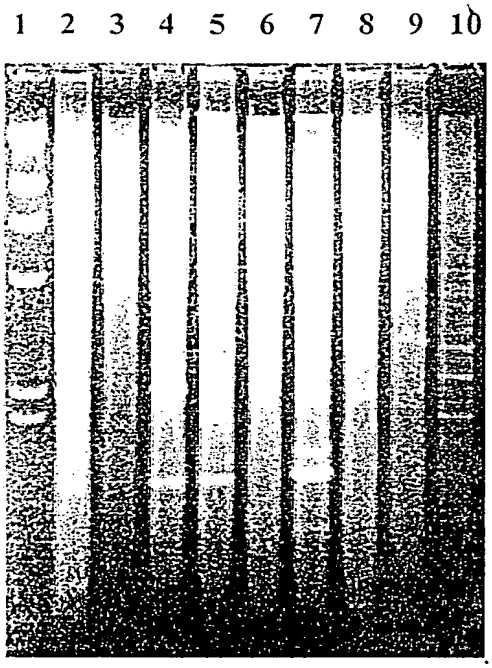

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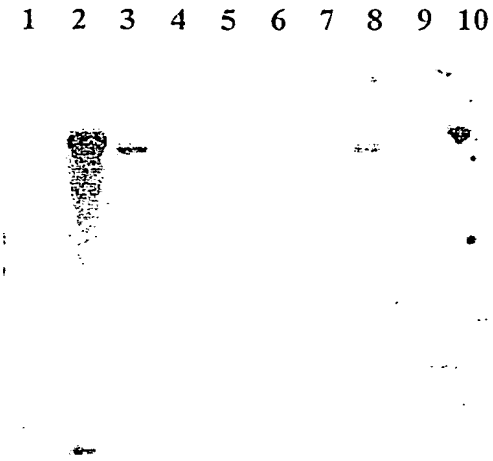

Fig. 2

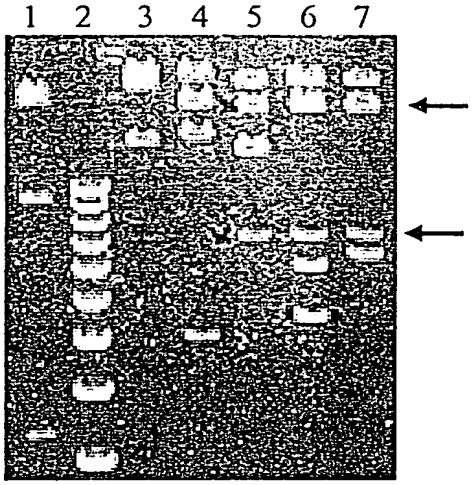

Fig. 3

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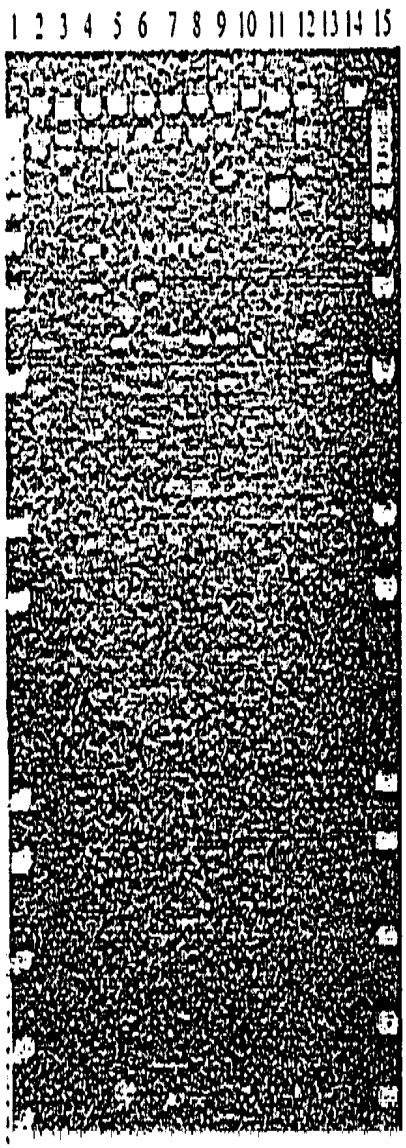

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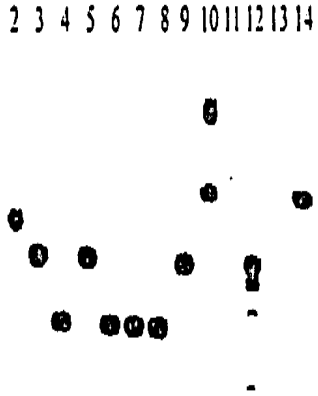

Fig. 4

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Fig. 4 (continued)

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Fig. 5

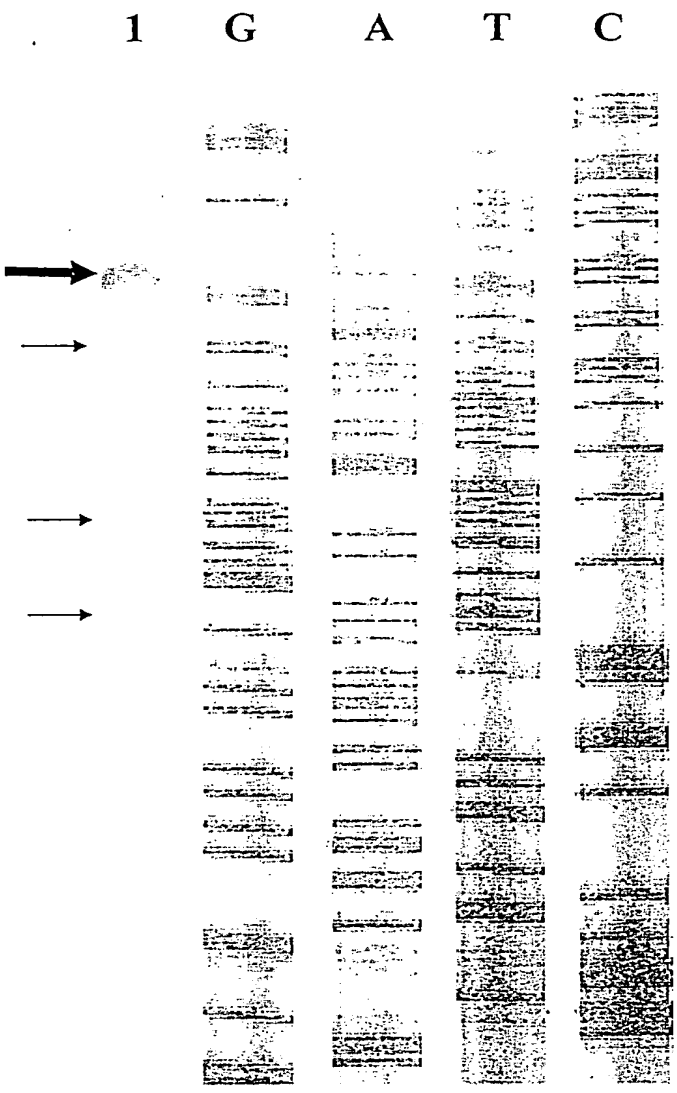

Fig. 6

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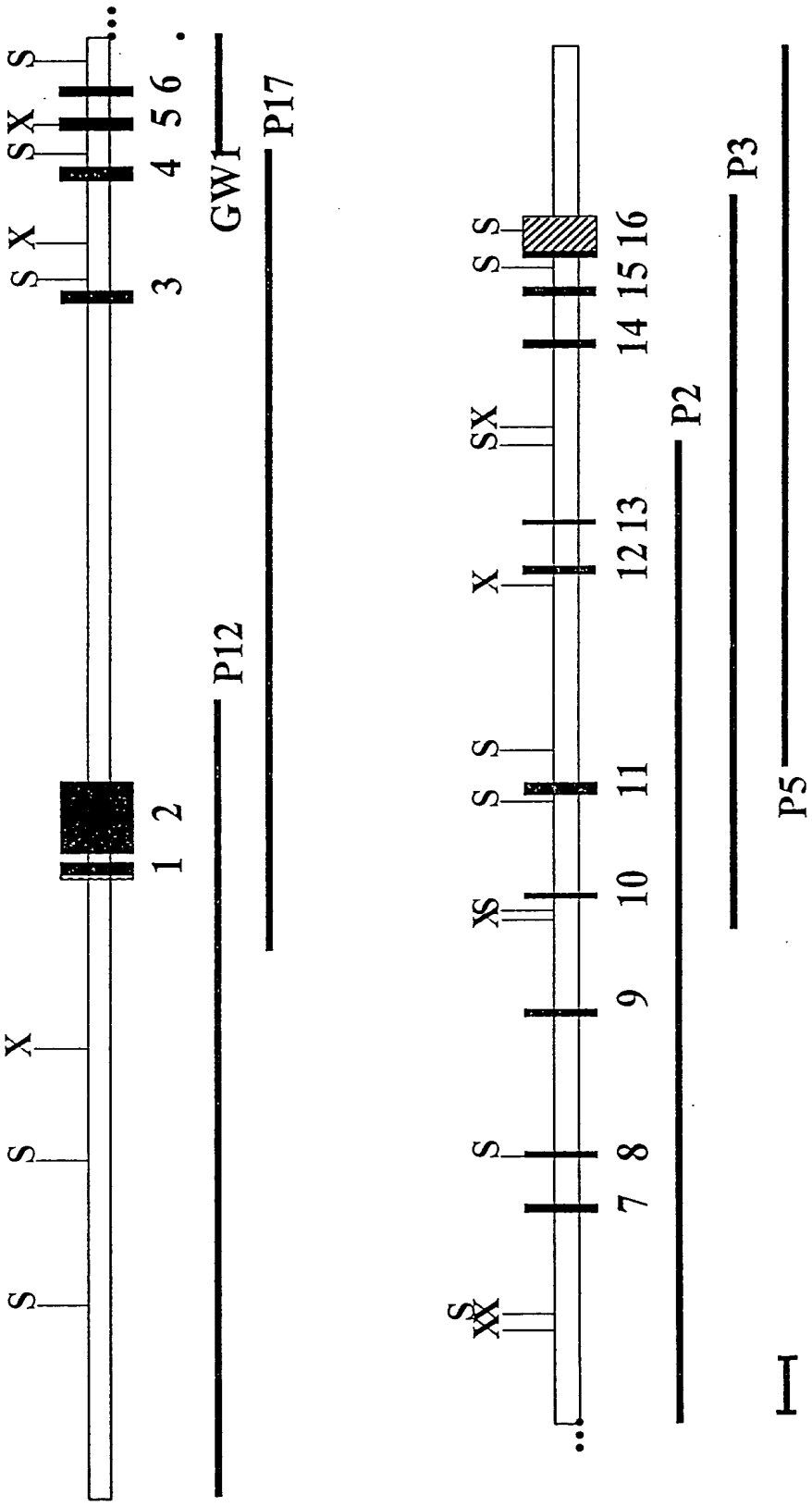

Fig. 7

Fig. 8A

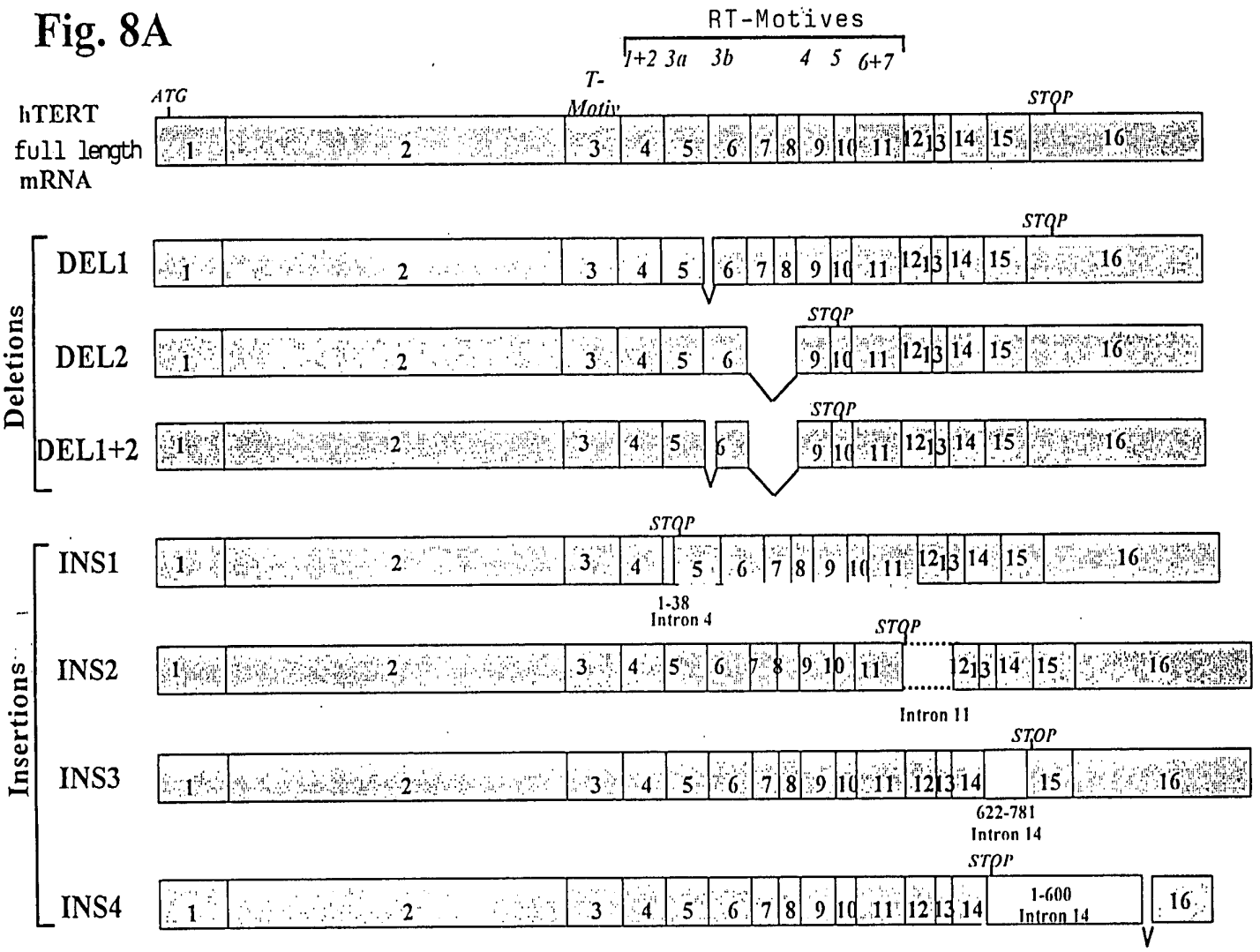
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Fig. 8B

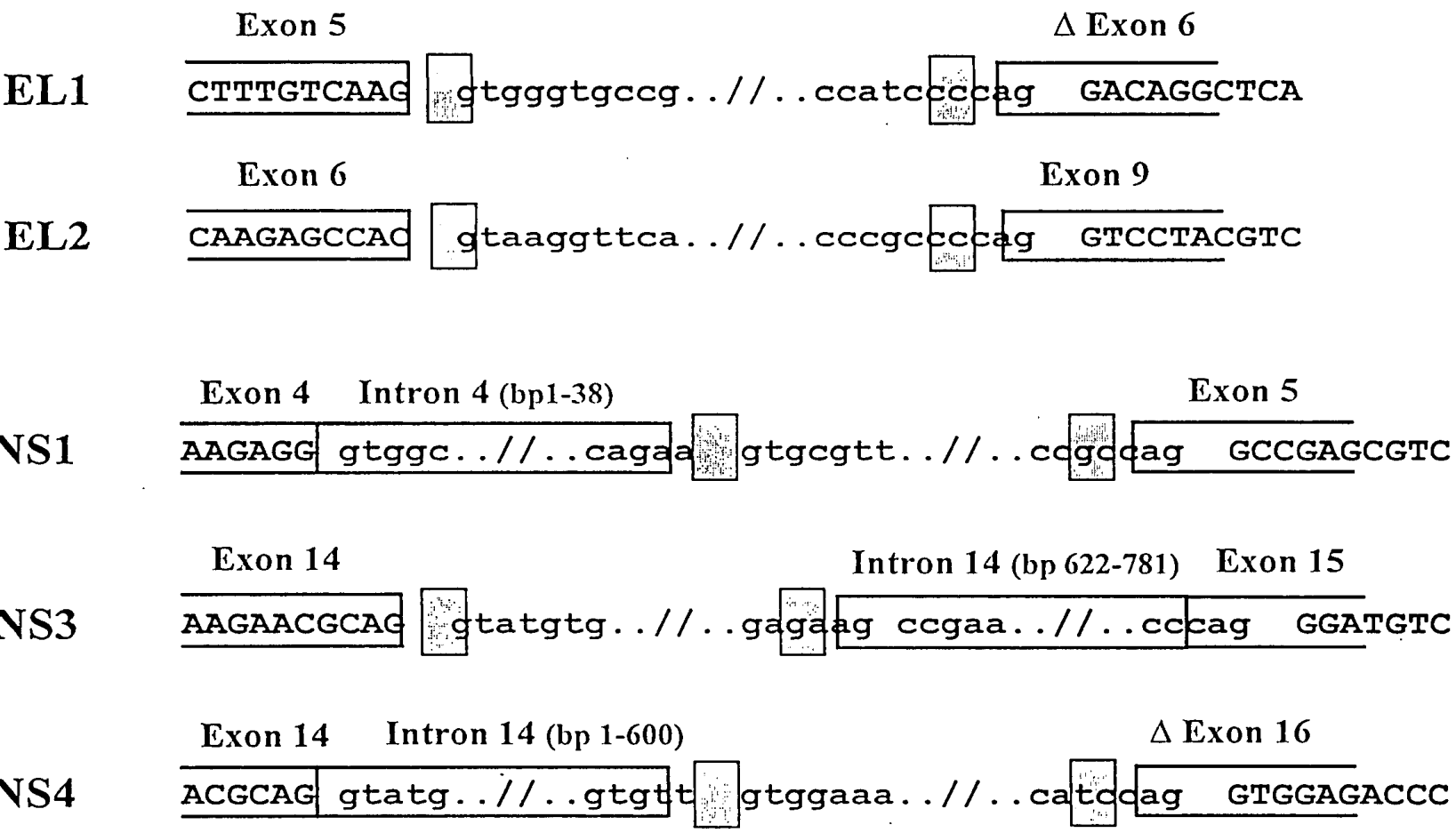
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Fig. 9

Fig. 10

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GCTCAAACTA CTCTATAAGA AAAACACCTA ATAAGCTGAT TTTCAAAAAT AAGCAAAAGA TCTGGGTAGA -7914
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GAGCAAGACT CCATCTCAAA ACAAAAACAA AAAAAAGAAG ATTAAAATTG TAATTTTTAT GTACCGTATA -6724
AATATATACT CTACTATATT AGAAGTTAAA AATTAAAACA ATTATAAAAG GTAATTAACC ACTTAATCTA -6654
AAATAAGAAC AATGTATGTG GGGTTTCTAG CTTCTGAAGA AGTAAAAGTT ATGGCCACGA TGGCAGAAAT -6584
```

Fig. 10

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GTGAGGAGGG AACAGTGGAA GTTACTGTTG TTAGACGCTC ATACTCTCTG TAAGTGACTT AATTTTAACC -6514
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CACCGTCCTC TCATTCACGG TGCTTTTTTT CTTGTGTGCT TGGAGATTTT CGATTGTGTG TTCGTGTTTG -6304
GTTAAACTTA ATCTGTATGA ATCCTGAAAC GAAAAATGGT GGTGATTTCC TCCAGAAGAA TTAGAGTACC -6234
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CAGGCACCCG CCACCATGCC CAGCTAATTT TTTGTATTTT TAGTAGAGAC GGGGGTGGGT GGGGTTCACC -1964
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Fig. 10


ATGTTGGCCA GGCTGGTCTC GAACTTCTGA CCTCAGATGA TCCACCTGCC TCTGCCTCCT AAAGTGCTGG -1894
GATTACAGGT GTGAGCCACC ATGCCCAGCT CAGAATTTAC TCTGTTTAGA AACATCTGGG TCTGAGGTAG -1824
CAAT-Box
GAAGCTCACC CCACTCAAGT GTTGTGGTGT TTTAAGCCAA TGATAGAATT TTTTTATTGT TGTTAGAACA -1754
CTCTTGATGT TTTACACTGT GATGACTAAG ACATCATCAG CTTTTCAAAG ACACACTAAC TGCACCCATA -1684
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Sp1
GCCCCTTTGC CCTAGTGGCA GAGACAATTC ACAAACACAG CCCTTTAAAA AGGCTTAGGG ATCACTAAGG -1404
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ACAGAGTGCC GGGGCCCAGG GTCAAGGCCG TTGTGGCTGG TGTGAGGCGC CCGGTGCGCG GCCAGCAGGA -844
CCAC-Box
Sp1
GCGCCTGGCT CCATTTCCCA CCCTTTCTCG ACGGGACCGC CCCGGTGGGT GATTAACAGA TTTGGGGTGG -774
TTTGCTCATG GTGGGGACCC CTCGCCGCCT GAGAACCTGC AAAGAGAAAT GACGGGCCTG TGTCAAGGAG -704
CCCAAGTCGC GGGGAAGTGT TGCAGGGAGG CACTCCGGGA GGTCCCGCGT GCCCGTCCAG GGAGCAATGC -634
AP-2
GTCCTCGGGT TCGTCCCCAG CCGCGTCTAC GCGCCTCCGT CCTCCCCTTC ACGTCCGGCA TTCGTGGTGC -564
CCGGAGCCCG ACGCCCCGCG TCCGGACCTG GAGGCAGCCC TGGGTCTCCG GATCAGGCCA GCGGCCAAAG -494
GGTCGCCGCA CGCACCTGTT CCCAGGGCCT CCACATCATG GCCCCTCCCT CGGGTTACCC CACAGCCTAG -424
Sp1
GCCGATTCGA CCTCTCTCCG CTGGGGCCCT CGCTGGCGTC CCTGCACCCT GGGAGCGCGA GCGGCGCGCG -354
Sp1
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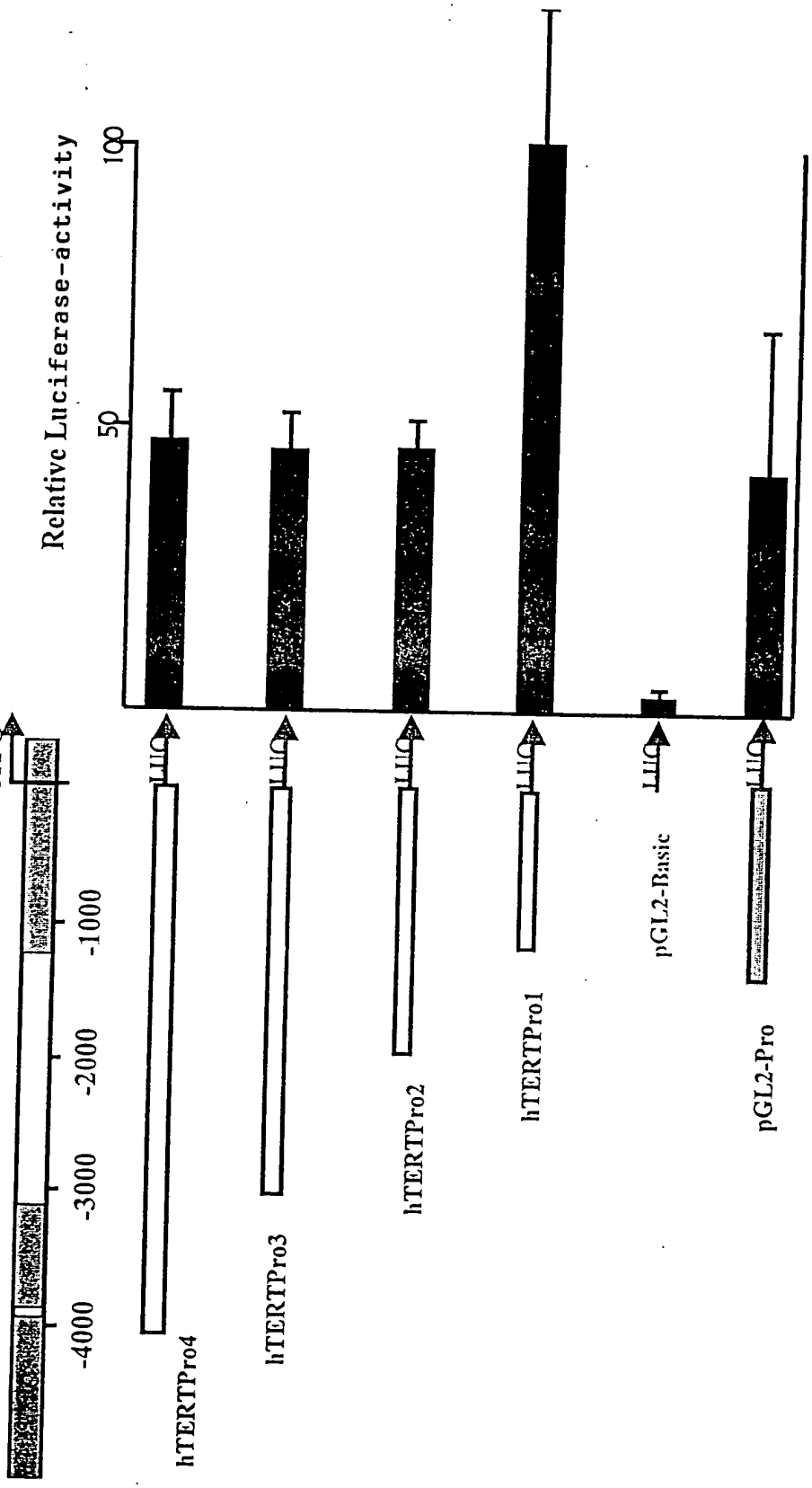
c-Myc
CCAGTGGATT CGCGGGCACA GACGCCCAGG ACCGCGCTCC CCACGTGGCG GAGGGACTGG GGACCCGGGC -214
Sp1
ACCCGTCCTG CCCCTTCACC TTCCAGCTCC GCCTCCTCCG CGCGGACCCC GCCCCGTCCC GACCCCTCCC -144
Sp1
GGGTCCCCGG CCCAGCCCCC TCCGGGCCCT CCCAGCCCCT CCCCTTCCTT TCCGCGGCCC CGCCCTCTCC -74
c-Myc
TCGCGGCGCG AGTTTCAGGC AGCGCTGCGT CCTGCTGCGC ACGTGGGAAG CCCTGGCCCC GGCCACCCCC -4
GCGATG 3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50
ATG
-4000
-3000
-2000
-1000
hTERTPro4
hTERTPro3
hTERTPro2
hTERTPro1
pGL2-Basic
pGL2-Pro

Fig.: 11